

Genome**L.K. Ashworth****A METRIC PHYSICAL MAP OF HUMAN CHROMOSOME 19**

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The chromosome 19 physical map constructed at Lawrence Livermore National Laboratory is a high resolution cosmid-based map spanning the entire chromosome. The foundation of the map consists of a set of 802 cosmid contigs assembled by automated restriction fragment analysis. These contigs span an estimated 54 Mb, or >95% of the chromosome excluding the centromere. Over 400 of the contigs have been mapped by fluorescence *in situ* hybridization (FISH) to metaphase bands. From these, 215 cosmids have been further ordered along the chromosome by a high resolution FISH mapping technique in which the distance between cosmid markers is also determined. This ordered FISH map provides a 'to-scale' framework, or metric map, upon which to anchor cosmid contigs. The average distance between these cosmid reference points is 230 Kb, with a range of 50-700 Kb. By identifying large insert clones (YACs, BACs, PACs and PIs) that span gaps between the ordered cosmid contigs, we have decreased the number of ordered islands to 63. These islands cover a cumulative length of 45 Mb, or about 90% of the non-centromeric part of the chromosome, with the largest island spanning 17 Mb. YACs have been identified by either of two procedures: STS screening of total genomic YAC libraries or hybridization of Alu-PCR products from cosmid contigs to Alu-PCR products from a chromosome 19-enriched YAC sub-library provided by Genethon. Large insert clones spanning gaps are being hybridized back to cosmid libraries to identify additional cosmids/contigs located in the gaps. Overlap between adjacent contigs in these regions can often be determined by EcoRI mapping. In some cases cosmid walking experiments are needed in order to achieve continuity at the cosmid level. To date, over 38 Mb of EcoRI restriction maps have been generated. In addition, over 400 genes and genetic markers have been localized on cosmids, of which nearly 300 have been incorporated into the ordered map. Genomic sequencing is being done in selected regions of interest particularly on three DNA repair genes found on the chromosome. Software has been designed that integrates and displays cosmid, YAC, FISH, and restriction maps, as well as sequence, hybridization, and screening data.

Work was performed by LLNL under the auspices of the U.S. DOE under contract No. W-7405-ENG-48.

Cold Spring Harbor Laboratory, Genome Mapping and Sequencing, Cold Spring Harbor, NY, May 10-14, 1995